# SEQUENCE LISTING

<110> POWDERJECT VACCINES, INC.

<120> METHOD

<130> 092633-0104

<140> PCT/US04/033391
<141> 2004-10-12

<150> 60/567,771
<151> 2004-05-05

<150> 60/526,571
<151> 2003-12-04

<150> 60/510,086
<151> 2003-10-10

<160> 19

<170> PatentIn Ver. 3.2

<210> 1
<211> 63
<212> PRT
<213> Influenza A virus

<400> 1
Met Lys Thr Ile Ile Ala Leu Ser Tyr Ile Leu Cys Leu Val Phe Ala
1 5 10 15

Gln Lys Leu Pro Gly Asn Asp Asn Ser Thr Ala Thr Leu Cys Leu Gly
20 25 30

His His Ala Val Ser Asn Gly Thr Leu Val Lys Thr Ile Thr Asn Asp
35 40 45

Gln Ile Glu Val Thr Asn Ala Thr Glu Leu Val Gln Ser Ser Ser
50 55 60

<210> 2
<211> 65
<212> PRT
<213> Influenza A virus

<400> 2
Met Ala Ser Lys Thr Ile Ile Ala Leu Ser Tyr Ile Leu Cys Leu Val
1 5 10 15

Phe Ala Gln Lys Leu Pro Gly Asn Asp Asn Ser Thr Ala Thr Leu Cys
20 25 30

Leu Gly His His Ala Val Ser Asn Gly Thr Leu Val Lys Thr Ile Thr
35 40 45

Asn Asp Gln Ile Glu Val Thr Asn Ala Thr Glu Leu Val Gln Ser Ser
50 55 60

Ser
65

<210> 3
<211> 62
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
consensus sequence

<400> 3
Lys Thr Ile Ile Ala Leu Ser Tyr Ile Leu Cys Leu Val Phe Ala Gln
1 5 10 15

Lys Leu Pro Gly Asn Asp Asn Ser Thr Ala Thr Leu Cys Leu Gly His
20 25 30

His Ala Val Ser Asn Gly Thr Leu Val Lys Thr Ile Thr Asn Asp Gln
35 40 45

Ile Glu Val Thr Asn Ala Thr Glu Leu Val Gln Ser Ser Ser
50 55 60

<210> 4
<211> 3759
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
nucleotide vector sequence

<400> 4
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agccgtttct gtaatgaagg agaaaactca ccgaggcagt tccataggat ggcaagatcc 180
tggtatcggt ctgcgattcc gactcgtcca acatcaatac aacctattaa tttcccctcg 240
tcaaaaataa ggttatcaag tgagaaatca ccatgagtga cgactgaatc cggtgagaat 300
ggcaaaagct tatgcatttc tttccagact tgttcaacag gccagccatt acgctcgtca 360
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aatacgcgat cgctgttaaa aggacaatta caaacaggaa tcgaatgcaa ccggcgcagg 480
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aatgctgttt tccccggggat cgcagtggtg agtaaccatg catcatcagg agtacggata 600
aaatgcttga tggtcggaag aggcataaat tccgtcagcc agtttagtct gaccatctca 660
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<210> 5
<211> 1503
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
nucleotide construct

<400> 5
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cttgaacggt ttgccgtgaa cccaggcctg ctggaaacat ctgagggatg tcgccagatc 180
ctggggcaat tgcagccatc cctccagacc gggagtgaag agctgaggtc cttgtataac 240
acagtggcta ccctctactg cgtacaccag aggatcgaga ttaaggatac caaggaggcc 300
ttggacaaaa ttgaggagga gcaaaacaag agcaagaaga aggcccagca ggcagctgct 360
gacactgggc atagcaacca ggtatcacag aactatccta ttgtccaaaa cattcagggc 420
cagatggttc atcaggccat cagcccccgg acgctcaatg cctgggtgaa ggttgtcgaa 480
gagaaggcct tttctcctga ggttatcccc atgttctccg ctttgagtga gggggccact 540
cctcaggacc tcaatacaat gcttaatacc gtgggcggcc atcaggccgc catgcaaatg 600
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ggcccaatcg cgcccggaca gatgcgggag cctcgcggct ctgacattgc cggcaccacc 720
tctacactgc aagagcaaat cggatggatg accaacaatc ctcccatccc agttggagaa 780
atctataaac ggtggatcat tctcggtctc aataaaattg ttagaatgta ctctccgaca 840
tccatccttg acattagaca gggacccaaa gagcctttta gggattacgt cgaccggttt 900
tataagaccc tgcgagcaga gcaggcctct caggaggtca aaaactggat gacggagaca 960
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gccaccctgg aagagatgat gaccgcctgt cagggagtag gcggacccgg acacaaagcc 1080
agagtgttgg ccgaagccat gagccaggtg acgaactccg caaccatcat gatgcagaga 1140
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accgcccgca actgtcgggc ccctaggaag aaagggtgtt ggaagtgcgg caaggaggga 1260
caccagatga aagactgtac agaacgacag gccaattttc ttggaaagat ttggccgagc 1320

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tacaagggga gacctggtaa tttcctgcaa agcaggcccg agcccaccgc ccccctgag 1380
gaatccttca ggtccggagt ggagaccaca acgcctcccc aaaaacagga accaatcgac 1440
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taa                                                               1503
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<210> 6
<211> 500
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic protein construct

<400> 6

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Glu Lys Ile Arg Leu Arg Pro Gly Gly Lys Lys Lys Tyr Lys Leu Lys
             20                  25                  30

His Ile Val Trp Ala Ser Arg Glu Leu Glu Arg Phe Ala Val Asn Pro
         35                  40                  45

Gly Leu Leu Glu Thr Ser Glu Gly Cys Arg Gln Ile Leu Gly Gln Leu
     50                  55                  60

Gln Pro Ser Leu Gln Thr Gly Ser Glu Glu Leu Arg Ser Leu Tyr Asn
 65                  70                  75                  80

Thr Val Ala Thr Leu Tyr Cys Val His Gln Arg Ile Glu Ile Lys Asp
                 85                  90                  95

Thr Lys Glu Ala Leu Asp Lys Ile Glu Glu Glu Gln Asn Lys Ser Lys
            100                 105                 110

Lys Lys Ala Gln Gln Ala Ala Ala Asp Thr Gly His Ser Asn Gln Val
        115                 120                 125

Ser Gln Asn Tyr Pro Ile Val Gln Asn Ile Gln Gly Gln Met Val His
    130                 135                 140

Gln Ala Ile Ser Pro Arg Thr Leu Asn Ala Trp Val Lys Val Val Glu
145                 150                 155                 160

Glu Lys Ala Phe Ser Pro Glu Val Ile Pro Met Phe Ser Ala Leu Ser
                165                 170                 175

Glu Gly Ala Thr Pro Gln Asp Leu Asn Thr Met Leu Asn Thr Val Gly
            180                 185                 190

Gly His Gln Ala Ala Met Gln Met Leu Lys Glu Thr Ile Asn Glu Glu
        195                 200                 205

Ala Ala Glu Trp Asp Arg Val His Pro Val His Ala Gly Pro Ile Ala
    210                 215                 220

Pro Gly Gln Met Arg Glu Pro Arg Gly Ser Asp Ile Ala Gly Thr Thr
225                 230                 235                 240

Ser Thr Leu Gln Glu Gln Ile Gly Trp Met Thr Asn Asn Pro Pro Ile
                245                 250                 255

Pro Val Gly Glu Ile Tyr Lys Arg Trp Ile Ile Leu Gly Leu Asn Lys
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            260                 265                 270

Ile Val Arg Met Tyr Ser Pro Thr Ser Ile Leu Asp Ile Arg Gln Gly
        275                 280                 285

Pro Lys Glu Pro Phe Arg Asp Tyr Val Asp Arg Phe Tyr Lys Thr Leu
    290                 295                 300

Arg Ala Glu Gln Ala Ser Gln Glu Val Lys Asn Trp Met Thr Glu Thr
305                 310                 315                 320

Leu Leu Val Gln Asn Ala Asn Pro Asp Cys Lys Thr Ile Leu Lys Ala
                325                 330                 335

Leu Gly Pro Ala Ala Thr Leu Glu Glu Met Met Thr Ala Cys Gln Gly
            340                 345                 350

Val Gly Gly Pro Gly His Lys Ala Arg Val Leu Ala Glu Ala Met Ser
        355                 360                 365

Gln Val Thr Asn Ser Ala Thr Ile Met Met Gln Arg Gly Asn Phe Arg
    370                 375                 380

Asn Gln Arg Lys Ile Val Lys Cys Phe Asn Cys Gly Lys Glu Gly His
385                 390                 395                 400

Thr Ala Arg Asn Cys Arg Ala Pro Arg Lys Lys Gly Cys Trp Lys Cys
                405                 410                 415

Gly Lys Glu Gly His Gln Met Lys Asp Cys Thr Glu Arg Gln Ala Asn
            420                 425                 430

Phe Leu Gly Lys Ile Trp Pro Ser Tyr Lys Gly Arg Pro Gly Asn Phe
        435                 440                 445

Leu Gln Ser Arg Pro Glu Pro Thr Ala Pro Pro Glu Glu Ser Phe Arg
    450                 455                 460

Ser Gly Val Glu Thr Thr Thr Pro Pro Gln Lys Gln Glu Pro Ile Asp
465                 470                 475                 480

Lys Glu Leu Tyr Pro Leu Thr Ser Leu Arg Ser Leu Phe Gly Asn Asp
                485                 490                 495

Pro Ser Ser Gln
            500
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<210> 7
<211> 1515
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic nucleotide construct

<400> 7
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ctagaacgat tcgcagttaa tcctggcctg ttagaaacat cagaaggctg tagacaaata 180
ctgggacagc tacaaccatc ccttcagaca ggatcagaag aacttagatc attatataat 240
acagtagcaa ccctctattg tgtgcatcaa aggatagaga taaaagacac caaggaagct 300
ttagacaaga tagaggaaga gcaaaacaaa agtaagaaaa aagcacagca agcagcagct 360
gacacaggac acagcaatca ggtcagccaa aattacccta tagtgcagaa catccagggg 420

caaatggtac atcaggccat atcacctaga actttaaatg catgggtaaa agtagtagaa 480
gagaaggctt tcagcccaga agtgataccc atgttttcag cattatcaga aggagccacc 540
ccacaagatt taaacaccat gctaaacaca gtgggggggac atcaagcagc catgcaaatg 600
ttaaaagaga ccatcaatga ggaagctgca gaatgggata gagtgcatcc agtgcatgca 660
gggcctattg caccaggcca gatgagagaa ccaaggggaa gtgacatagc aggaactact 720
agtacccttc aggaacaaat aggatggatg acaaataatc cacctatccc agtaggagaa 780
atttataaaa gatggataat cctgggatta aataaaatag taagaatgta tagccctacc 840
agcattctgg acataagaca aggaccaaaa gaacccttta gagactatgt agaccggttc 900
tataaaactc taagagccga gcaagcttca caggaggtaa aaaattggat gacagaaacc 960
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ttcaagaact gctga 1515

<210> 8
<211> 504
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
protein construct

<400> 8
Met Gly Ala Arg Ala Ser Val Leu Ser Gly Gly Glu Leu Asp Arg Trp
1 5 10 15

Glu Lys Ile Arg Leu Arg Pro Gly Gly Lys Lys Lys Tyr Lys Leu Lys
20 25 30

His Ile Val Trp Ala Ser Arg Glu Leu Glu Arg Phe Ala Val Asn Pro
35 40 45

Gly Leu Leu Glu Thr Ser Glu Gly Cys Arg Gln Ile Leu Gly Gln Leu
50 55 60

Gln Pro Ser Leu Gln Thr Gly Ser Glu Glu Leu Arg Ser Leu Tyr Asn
65 70 75 80

Thr Val Ala Thr Leu Tyr Cys Val His Gln Arg Ile Glu Ile Lys Asp
85 90 95

Thr Lys Glu Ala Leu Asp Lys Ile Glu Glu Glu Gln Asn Lys Ser Lys
100 105 110

Lys Lys Ala Gln Gln Ala Ala Ala Asp Thr Gly His Ser Asn Gln Val
115 120 125

Ser Gln Asn Tyr Pro Ile Val Gln Asn Ile Gln Gly Gln Met Val His
130 135 140

Gln Ala Ile Ser Pro Arg Thr Leu Asn Ala Trp Val Lys Val Val Glu
145 150 155 160

Glu Lys Ala Phe Ser Pro Glu Val Ile Pro Met Phe Ser Ala Leu Ser
165 170 175

Glu Gly Ala Thr Pro Gln Asp Leu Asn Thr Met Leu Asn Thr Val Gly

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            180                 185                 190

Gly His Gln Ala Ala Met Gln Met Leu Lys Glu Thr Ile Asn Glu Glu
        195                 200                 205

Ala Ala Glu Trp Asp Arg Val His Pro Val His Ala Gly Pro Ile Ala
    210                 215                 220

Pro Gly Gln Met Arg Glu Pro Arg Gly Ser Asp Ile Ala Gly Thr Thr
225                 230                 235                 240

Ser Thr Leu Gln Glu Gln Ile Gly Trp Met Thr Asn Asn Pro Pro Ile
                245                 250                 255

Pro Val Gly Glu Ile Tyr Lys Arg Trp Ile Ile Leu Gly Leu Asn Lys
            260                 265                 270

Ile Val Arg Met Tyr Ser Pro Thr Ser Ile Leu Asp Ile Arg Gln Gly
        275                 280                 285

Pro Lys Glu Pro Phe Arg Asp Tyr Val Asp Arg Phe Tyr Lys Thr Leu
    290                 295                 300

Arg Ala Glu Gln Ala Ser Gln Glu Val Lys Asn Trp Met Thr Glu Thr
305                 310                 315                 320

Leu Leu Val Gln Asn Ala Asn Pro Asp Cys Lys Thr Ile Leu Lys Ala
                325                 330                 335

Leu Gly Pro Ala Ala Thr Leu Glu Glu Met Met Thr Ala Cys Gln Gly
            340                 345                 350

Val Gly Gly Pro Gly His Lys Ala Arg Val Leu Val Gly Phe Pro Val
        355                 360                 365

Thr Pro Gln Val Pro Leu Arg Pro Met Thr Tyr Lys Ala Ala Val Asp
    370                 375                 380

Leu Ser His Phe Leu Lys Glu Lys Gly Gly Leu Glu Gly Leu Ile His
385                 390                 395                 400

Ser Gln Arg Arg Gln Asp Ile Leu Asp Leu Trp Ile Tyr His Thr Gln
                405                 410                 415

Gly Tyr Phe Pro Asp Trp Gln Asn Tyr Thr Pro Gly Pro Gly Val Arg
            420                 425                 430

Tyr Pro Leu Thr Phe Gly Trp Cys Tyr Lys Leu Val Pro Val Glu Pro
        435                 440                 445

Asp Lys Val Glu Glu Ala Asn Lys Gly Glu Asn Thr Ser Leu Leu His
    450                 455                 460

Pro Val Ser Leu His Gly Met Asp Asp Pro Glu Arg Glu Val Leu Glu
465                 470                 475                 480

Trp Arg Phe Asp Ser His Leu Ala Phe His His Val Ala Arg Glu Leu
                485                 490                 495

His Pro Glu Tyr Phe Lys Asn Cys
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<210> 9
<211> 1518

<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
nucleotide construct

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ggcccaatcg cgcccggaca gatgcgggag cctcgcggct ctgacattgc cggcaccacc 720
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aaggcagctg tagatcttag ccacttttta aaagaaaagg ggggactgga agggctaatt 1200
cactcccaaa gaagacaaga tatccttgat ctgtggatct accacacaca aggctacttc 1260
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accagcttgt tacaccctgt gagcctgcat gggatggatg acccggagag agaagtgtta 1440
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<210> 10
<211> 505
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
protein construct

<400> 10
Met Gly Ala Arg Ala Ser Val Leu Ser Gly Gly Glu Leu Asp Arg Trp
1 5 10 15

Glu Lys Ile Arg Leu Arg Pro Gly Gly Lys Lys Lys Tyr Lys Leu Lys
20 25 30

His Ile Val Trp Ala Ser Arg Glu Leu Glu Arg Phe Ala Val Asn Pro
35 40 45

Gly Leu Leu Glu Thr Ser Glu Gly Cys Arg Gln Ile Leu Gly Gln Leu
50 55 60

Gln Pro Ser Leu Gln Thr Gly Ser Glu Glu Leu Arg Ser Leu Tyr Asn
65 70 75 80

Thr Val Ala Thr Leu Tyr Cys Val His Gln Arg Ile Glu Ile Lys Asp
85 90 95

Thr Lys Glu Ala Leu Asp Lys Ile Glu Glu Glu Gln Asn Lys Ser Lys

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            100                 105                 110

Lys Lys Ala Gln Gln Ala Ala Ala Asp Thr Gly His Ser Asn Gln Val
        115                 120                 125

Ser Gln Asn Tyr Pro Ile Val Gln Asn Ile Gln Gly Gln Met Val His
    130                 135                 140

Gln Ala Ile Ser Pro Arg Thr Leu Asn Ala Trp Val Lys Val Val Glu
145                 150                 155                 160

Glu Lys Ala Phe Ser Pro Glu Val Ile Pro Met Phe Ser Ala Leu Ser
                165                 170                 175

Glu Gly Ala Thr Pro Gln Asp Leu Asn Thr Met Leu Asn Thr Val Gly
            180                 185                 190

Gly His Gln Ala Ala Met Gln Met Leu Lys Glu Thr Ile Asn Glu Glu
        195                 200                 205

Ala Ala Glu Trp Asp Arg Val His Pro Val His Ala Gly Pro Ile Ala
    210                 215                 220

Pro Gly Gln Met Arg Glu Pro Arg Gly Ser Asp Ile Ala Gly Thr Thr
225                 230                 235                 240

Ser Thr Leu Gln Glu Gln Ile Gly Trp Met Thr Asn Asn Pro Pro Ile
                245                 250                 255

Pro Val Gly Glu Ile Tyr Lys Arg Trp Ile Ile Leu Gly Leu Asn Lys
            260                 265                 270

Ile Val Arg Met Tyr Ser Pro Thr Ser Ile Leu Asp Ile Arg Gln Gly
        275                 280                 285

Pro Lys Glu Pro Phe Arg Asp Tyr Val Asp Arg Phe Tyr Lys Thr Leu
    290                 295                 300

Arg Ala Glu Gln Ala Ser Gln Glu Val Lys Asn Trp Met Thr Glu Thr
305                 310                 315                 320

Leu Leu Val Gln Asn Ala Asn Pro Asp Cys Lys Thr Ile Leu Lys Ala
                325                 330                 335

Leu Gly Pro Ala Ala Thr Leu Glu Glu Met Met Thr Ala Cys Gln Gly
            340                 345                 350

Val Gly Gly Pro Gly His Lys Ala Arg Val Leu Met Val Gly Phe Pro
        355                 360                 365

Val Thr Pro Gln Val Pro Leu Arg Pro Met Thr Tyr Lys Ala Ala Val
    370                 375                 380

Asp Leu Ser His Phe Leu Lys Glu Lys Gly Gly Leu Glu Gly Leu Ile
385                 390                 395                 400

His Ser Gln Arg Arg Gln Asp Ile Leu Asp Leu Trp Ile Tyr His Thr
                405                 410                 415

Gln Gly Tyr Phe Pro Asp Trp Gln Asn Tyr Thr Pro Gly Pro Gly Val
            420                 425                 430

Arg Tyr Pro Leu Thr Phe Gly Trp Cys Tyr Lys Leu Val Pro Val Glu
        435                 440                 445
```

```
Pro Asp Lys Val Glu Glu Ala Asn Lys Gly Glu Asn Thr Ser Leu Leu
    450                 455                 460

His Pro Val Ser Leu His Gly Met Asp Asp Pro Glu Arg Glu Val Leu
465                 470                 475                 480

Glu Trp Arg Phe Asp Ser His Leu Ala Phe His His Val Ala Arg Glu
                485                 490                 495

Leu His Pro Glu Tyr Phe Lys Asn Cys
            500                 505
```

<210> 11
<211> 1689
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic nucleotide construct

<400> 11
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atgggcccca tcagtcccat cgagaccgtg ccggtgaagc tgaaacccgg gatggacggc 60
cccaaggtca agcagtggcc actcaccgag gagaagatca aggccctggt ggagatctgc 120
accgagatgg agaaagaggg caagatcagc aagatcgggc ctgagaaccc atacaacacc 180
cccgtgtttg ccatcaagaa gaaggacagc accaagtggc gcaagctggt ggatttccgg 240
gagctgaata agcggaccca ggatttctgg gaggtccagc tgggcatccc ccatccggcc 300
ggcctgaaga agaagaagag cgtgaccgtg ctggacgtgg gcgacgctta cttcagcgtc 360
cctctggacg aggactttag aaagtacacc gcctttacca tcccatctat caacaacgag 420
acccctggca tcagatatca gtacaacgtc ctcccccagg gctggaaggg ctctcccgcc 480
attttccaga gctccatgac caagatcctg gagccgtttc ggaagcagaa ccccgatatc 540
gtcatctacc agtacatgga cgacctgtac gtgggctctg acctggaaat cgggcagcat 600
cgcacgaaga ttgaggagct gaggcagcat ctgctgagat ggggcctgac cactccggac 660
aagaagcatc agaaggagcc gccattcctg tggatgggct acgagctcca tcccgacaag 720
tggaccgtgc agcctatcgt cctccccgag aaggacagct ggaccgtgaa cgacatccag 780
aagctggtgg gcaagctcaa ctgggctagc cagatctatc ccgggatcaa ggtgcgccag 840
ctctgcaagc tgctgcgcgg caccaaggcc ctgaccgagg tgattccgct cacggaggaa 900
gccgagctcg agctggctga gaaccgggag atcctgaagg agcccgtgca cggcgtgtac 960
tatgaccgct ccaaggacct gatcgccgaa atccagaagc agggccaggg gcagtggaca 1020
taccagattt accaggagcc tttcaagaac ctcaagaccg gcaagtacgc ccgcatgagg 1080
ggcgcccaca ccaacgatgt caagcagctg accgaggccg tccagaagat cacgaccgag 1140
tccatcgtga tctgggggaa gacacccaag ttcaagctgc ctatccagaa ggagacctgg 1200
gagacgtggt ggaccgaata ttggcaggcc acctggattc ccgagtggga gttcgtgaat 1260
acacctcctc tggtgaagct gtggtaccag ctcgagaagg agcccatcgt gggcgcggag 1320
acattctacg tggacggcgc ggccaaccgc gaaacaaagc tcgggaaggc cgggtacgtc 1380
accaaccggg gccgccagaa ggtcgtcacc ctgaccgaca ccaccaacca gaagacggag 1440
ctgcaggcca tctatctcgc tctccaggac tccggcctgg aggtgaacat cgtgacggac 1500
agccagtacg cgctgggcat tattcaggcc cagccggacc agtccgagag cgaactggtg 1560
aaccagatta tcgagcagct gatcaagaaa gagaaggtct acctcgcctg ggtcccggcc 1620
cataagggca ttggcggcaa cgagcaggtc gacaagctgg tgagtgcggg gattagaaag 1680
gtgctgtaa                                                        1689
```

<210> 12
<211> 562
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic protein construct

<400> 12
```
Met Gly Pro Ile Ser Pro Ile Glu Thr Val Ser Val Lys Leu Lys Pro
```

```
  1               5                  10                  15

Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu Lys
            20                  25                  30

Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Met Glu Lys Glu Gly Lys
        35                  40                  45

Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe Ala
    50                  55                  60

Ile Lys Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe Arg
65                  70                  75                  80

Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly Ile
                85                  90                  95

Pro His Pro Ala Gly Leu Lys Lys Lys Lys Ser Val Thr Val Leu Asp
            100                 105                 110

Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Glu Asp Phe Arg Lys
        115                 120                 125

Tyr Thr Ala Phe Thr Ile Pro Ser Ile Asn Asn Glu Thr Pro Gly Ile
    130                 135                 140

Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro Ala
145                 150                 155                 160

Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys Gln
                165                 170                 175

Asn Pro Asp Ile Val Ile Tyr Gln Tyr Met Asp Asp Leu Tyr Val Gly
            180                 185                 190

Ser Asp Leu Glu Ile Gly Gln His Arg Thr Lys Ile Glu Glu Leu Arg
        195                 200                 205

Gln His Leu Leu Arg Trp Gly Leu Thr Thr Pro Asp Lys Lys His Gln
    210                 215                 220

Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp Lys
225                 230                 235                 240

Trp Thr Val Gln Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Thr Val
                245                 250                 255

Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln Ile
            260                 265                 270

Tyr Pro Gly Ile Lys Val Arg Gln Leu Cys Lys Leu Leu Arg Gly Thr
        275                 280                 285

Lys Ala Leu Thr Glu Val Ile Pro Leu Thr Glu Glu Ala Glu Leu Glu
    290                 295                 300

Leu Ala Glu Asn Arg Glu Ile Leu Lys Glu Pro Val His Gly Val Tyr
305                 310                 315                 320

Tyr Asp Pro Ser Lys Asp Leu Ile Ala Glu Ile Gln Lys Gln Gly Gln
                325                 330                 335

Gly Gln Trp Thr Tyr Gln Ile Tyr Gln Glu Pro Phe Lys Asn Leu Lys
            340                 345                 350
```

```
Thr Gly Lys Tyr Ala Arg Met Arg Gly Ala His Thr Asn Asp Val Lys
        355                 360                 365

Gln Leu Thr Glu Ala Val Gln Lys Ile Thr Thr Glu Ser Ile Val Ile
    370                 375                 380

Trp Gly Lys Thr Pro Lys Phe Lys Leu Pro Ile Gln Lys Glu Thr Trp
385                 390                 395                 400

Glu Thr Trp Trp Thr Glu Tyr Trp Gln Ala Thr Trp Ile Pro Glu Trp
                405                 410                 415

Glu Phe Val Asn Thr Pro Pro Leu Val Lys Leu Trp Tyr Gln Leu Glu
            420                 425                 430

Lys Glu Pro Ile Val Gly Ala Glu Thr Phe Tyr Val Asp Gly Ala Ala
        435                 440                 445

Asn Arg Glu Thr Lys Leu Gly Lys Ala Gly Tyr Val Thr Asn Arg Gly
    450                 455                 460

Arg Gln Lys Val Val Thr Leu Thr Asp Thr Thr Asn Gln Lys Thr Glu
465                 470                 475                 480

Leu Gln Ala Ile Tyr Leu Ala Leu Gln Asp Ser Gly Leu Glu Val Asn
                485                 490                 495

Ile Val Thr Asp Ser Gln Tyr Ala Leu Gly Ile Ile Gln Ala Gln Pro
            500                 505                 510

Asp Gln Ser Glu Ser Glu Leu Val Asn Gln Ile Ile Glu Gln Leu Ile
        515                 520                 525

Lys Lys Glu Lys Val Tyr Leu Ala Trp Val Pro Ala His Lys Gly Ile
    530                 535                 540

Gly Gly Asn Glu Gln Val Asp Lys Leu Val Ser Ala Gly Ile Arg Lys
545                 550                 555                 560

Val Leu
```

<210> 13
<211> 1689
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic nucleotide construct

<400> 13
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atgggcccca tcagtcccat cgagaccgtg ccggtgaagc tgaaacccgg gatggacggc 60
cccaaggtca agcagtggcc actcaccgag gagaagatca aggccctggt ggagatctgc 120
accgagatgg agaaagaggg caagatcagc aagatcgggc ctgagaaccc atacaacacc 180
cccgtgtttg ccatcaagaa gaaggacagc accaagtggc gcaagctggt ggatttccgg 240
gagctgaata agcggaccca ggatttctgg gaggtccagc tgggcatccc ccatccggcc 300
ggcctgaaga agaagaagag cgtgaccgtg ctggacgtgg gcgacgctta cttcagcgtc 360
cctctggacg aggactttag aaagtacacc gcctttacca tcccatctat caacaacgag 420
acccctggca tcagatatca gtacaacgtc ctcccccagg gctggaaggg ctctcccgcc 480
attttccaga gctccatgac caagatcctg gagccgtttc ggaagcagaa ccccgatatc 540
gtcatctacc agtacatgga cgacctgtac gtgggctctg acctggaaat cgggcagcat 600
cgcacgaaga ttgaggagct gaggcagcat ctgctgagat ggggcctgac cactccggac 660
aagaagcatc agaaggagcc gccattcctg tggatgggct acgagctcca tcccgacaag 720
```

```
tggaccgtgc agcctatcgt cctccccgag aaggacagct ggaccgtgaa cgacatccag 780
aagctggtgg gcaagctcaa ctgggctagc cagatctatc ccgggatcaa ggtgcgccag 840
ctctgcaagc tgctgcgcgg caccaaggcc ctgaccgagg tgattccccc cacggaggaa 900
gccgagctcg agctggctga gaaccgggag atcctgaagg agcccgtgca cggcgtgtac 960
tatgaccccc ccaaggacct gatcgccgaa atccagaagc agggccaggg gcagtggaca 1020
taccagattt accaggagcc tttcaagaac ctcaagaccg gcaagtacgc ccgcatgagg 1080
ggcgcccaca ccaacgatgt caagcagctg accgaggccg tccagaagat cacgaccgag 1140
tccatcgtga tctgggggaa gacacccaag ttcaagctgc ctatccagaa ggagacctgg 1200
gagacgtggt ggaccgaata ttggcaggcc acctggattc ccgagtggga gttcgtgaat 1260
acacctcctc tggtgaagct gtggtaccag ctcgagaagg agcccatcgt gggcgcggag 1320
acattctacg tggacggcgc ggccaaccgc gaaacaaagc tcgggaaggc cgggtacgtc 1380
accaaccggg gccgccagaa ggtcgtcacc ctgaccgaca ccaccaacca gaagacggag 1440
ctgcaggcca tctatctcgc tctccaggac tccggcctgg aggtgaacat cgtgacggac 1500
agccagtacg cgctgggcat tattcaggcc cagccggacc agtccgagag cgaactggtg 1560
aaccagatta tcgagcagct gatcaagaaa gagaaggtct acctcgcctg ggtcccggcc 1620
cataagggca ttggcggcaa cgagcaggtc gacaagctgg tgagtgcggg gattagaaag 1680
gtgctgtaa                                                        1689
```

<210> 14
<211> 562
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic protein construct

<400> 14

```
Met Gly Pro Ile Ser Pro Ile Glu Thr Val Ser Val Lys Leu Lys Pro
  1               5                  10                  15

Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu Lys
             20                  25                  30

Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Met Glu Lys Glu Gly Lys
         35                  40                  45

Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe Ala
     50                  55                  60

Ile Lys Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe Arg
 65                  70                  75                  80

Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly Ile
                 85                  90                  95

Pro His Pro Ala Gly Leu Lys Lys Lys Lys Ser Val Thr Val Leu Asp
            100                 105                 110

Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Glu Asp Phe Arg Lys
        115                 120                 125

Tyr Thr Ala Phe Thr Ile Pro Ser Ile Asn Asn Glu Thr Pro Gly Ile
    130                 135                 140

Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro Ala
145                 150                 155                 160

Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys Gln
                165                 170                 175

Asn Pro Asp Ile Val Ile Tyr Gln Tyr Met Asp Asp Leu Tyr Val Gly
            180                 185                 190
```

```
Ser Asp Leu Glu Ile Gly Gln His Arg Thr Lys Ile Glu Glu Leu Arg
        195                 200                 205

Gln His Leu Leu Arg Trp Gly Leu Thr Thr Pro Asp Lys Lys His Gln
    210                 215                 220

Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp Lys
225                 230                 235                 240

Trp Thr Val Gln Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Thr Val
                245                 250                 255

Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln Ile
            260                 265                 270

Tyr Pro Gly Ile Lys Val Arg Gln Leu Cys Lys Leu Leu Arg Gly Thr
        275                 280                 285

Lys Ala Leu Thr Glu Val Ile Pro Leu Thr Glu Glu Ala Glu Leu Glu
    290                 295                 300

Leu Ala Glu Asn Arg Glu Ile Leu Lys Glu Pro Val His Gly Val Tyr
305                 310                 315                 320

Tyr Asp Pro Ser Lys Asp Leu Ile Ala Glu Ile Gln Lys Gln Gly Gln
                325                 330                 335

Gly Gln Trp Thr Tyr Gln Ile Tyr Gln Glu Pro Phe Lys Asn Leu Lys
            340                 345                 350

Thr Gly Lys Tyr Ala Arg Met Arg Gly Ala His Thr Asn Asp Val Lys
        355                 360                 365

Gln Leu Thr Glu Ala Val Gln Lys Ile Thr Thr Glu Ser Ile Val Ile
    370                 375                 380

Trp Gly Lys Thr Pro Lys Phe Lys Leu Pro Ile Gln Lys Glu Thr Trp
385                 390                 395                 400

Glu Thr Trp Trp Thr Glu Tyr Trp Gln Ala Thr Trp Ile Pro Glu Trp
                405                 410                 415

Glu Phe Val Asn Thr Pro Pro Leu Val Lys Leu Trp Tyr Gln Leu Glu
            420                 425                 430

Lys Glu Pro Ile Val Gly Ala Glu Thr Phe Tyr Val Asp Gly Ala Ala
        435                 440                 445

Asn Arg Glu Thr Lys Leu Gly Lys Ala Gly Tyr Val Thr Asn Arg Gly
    450                 455                 460

Arg Gln Lys Val Val Thr Leu Thr Asp Thr Thr Asn Gln Lys Thr Glu
465                 470                 475                 480

Leu Gln Ala Ile Tyr Leu Ala Leu Gln Asp Ser Gly Leu Glu Val Asn
                485                 490                 495

Ile Val Thr Asp Ser Gln Tyr Ala Leu Gly Ile Ile Gln Ala Gln Pro
            500                 505                 510

Asp Gln Ser Glu Ser Glu Leu Val Asn Gln Ile Ile Glu Gln Leu Ile
        515                 520                 525

Lys Lys Glu Lys Val Tyr Leu Ala Trp Val Pro Ala His Lys Gly Ile
    530                 535                 540
```

Gly Gly Asn Glu Gln Val Asp Lys Leu Val Ser Ala Gly Ile Arg Lys
545 550 555 560

Val Leu

<210> 15
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 15
Ile Pro Gln Ser Leu Asp Ser Trp Trp Thr Ser Leu
1 5 10

<210> 16
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 16
Arg Ile Gln Arg Gly Pro Gly Arg Ala Phe Val Ile Thr Gly Lys
1 5 10 15

<210> 17
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic primer

<400> 17
cgccactctc ttccgacacc 20

<210> 18
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic primer

<400> 18
ccaagaacat cacacggaac c 21

<210> 19
<211> 9
<212> PRT

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 19
His Gly Pro Ser Leu Tyr Arg Thr Phe
1 5